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PAGE: 1

RAW SEQUENCE LISTING
PATENT APPLICATION *US/08/404,832*

DATE: 04/05/95
TIME: 10:08:49

INPUT SET: S3120.raw

> This Raw Listing contains the General
> Information Section and up to the first 5 pages.

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 1                          SEQUENCE LISTING
 2
 3   (1)    General Information:
 4
 5        (i) APPLICANT: DIXIT, VISHA M.
 6
 7       (ii) TITLE OF INVENTION: CD40 BINDING COMPOSITIONS AND METHODS OF
 8              USING SAME
 9
10      (iii) NUMBER OF SEQUENCES: 12
11
12       (iv) CORRESPONDENCE ADDRESS:
13              (A) ADDRESSEE: MORRISON & FOERSTER
14              (B) STREET: 755 Page Mill Road
15              (C) CITY: Palo Alto
16              (D) STATE: California
17              (E) COUNTRY: USA
18              (F) ZIP: 94304-1018
19
20        (v) COMPUTER READABLE FORM:
21              (A) MEDIUM TYPE: Floppy disk
22              (B) COMPUTER: IBM PC compatible
23              (C) OPERATING SYSTEM: PC-DOS/MS-DOS
24              (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
25
26       (vi) CURRENT APPLICATION DATA:
27              (A) APPLICATION NUMBER: US
28              (B) FILING DATE:
29              (C) CLASSIFICATION:
30
31     (viii) ATTORNEY/AGENT INFORMATION:
32              (A) NAME: KONSKI, ANTOINETTE F.
33              (B) REGISTRATION NUMBER: 34,202
34              (C) REFERENCE/DOCKET NUMBER: 203442102500
35
36       (ix) TELECOMMUNICATION INFORMATION:
37              (A) TELEPHONE: (415) 813-5600
38              (B) TELEFAX: (415) 494-0792
39              (C) TELEX: 706141
40
41
42   (2) INFORMATION FOR SEQ ID NO:1:
43
44        (i) SEQUENCE CHARACTERISTICS:
45              (A) LENGTH: 2339 base pairs
46              (B) TYPE: nucleic acid
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INPUT SET: S3120.raw

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47                  (C) STRANDEDNESS: single
48                  (D) TOPOLOGY: linear
49
50
51
52        (ix) FEATURE:
53                  (A) NAME/KEY: CDS
54                  (B) LOCATION: 211..1911
55
56
57        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
58
59   ACGAAGGCCA CGCGCCCGGC GCCCCTGAGC CGGCCGAGCG GCGACGGACC GCGAGATGAG        60
60
61   GAAAATGAGG CCCAAAGAAG TGATGCCACT TGGTTAAGGT CCCAGAGCAG GTCAGAATCA       120
62
63   GACCTAGGAT CAGAAACCTG GCTCCTGGCT CCTGCTCCCT ACTCTTCTAA GGATCGCTGT       180
64
65   CCTGACAGAA GAGAACTCCT CTTTCCTAAA ATG GAG TCG AGT AAA AAG ATG GAC       234
66                                    Met Glu Ser Ser Lys Lys Met Asp
67                                     1               5
68
69   TCT CCT GGC GCG CTG CAG ACT AAC CCG CCG CTA AAG CTG CAC ACT GAC       282
70   Ser Pro Gly Ala Leu Gln Thr Asn Pro Pro Leu Lys Leu His Thr Asp
71        10              15                  20
72
73   CGC AGT GCT GGG ACG CCA GTT TTT GTC CCT GAA CAA GGA GGT TAC AAG       330
74   Arg Ser Ala Gly Thr Pro Val Phe Val Pro Glu Gln Gly Gly Tyr Lys
75   25              30                  35                  40
76
77   GAA AAG TTT GTG AAG ACC GTG GAG GAC AAG TAC AAG TGT GAG AAG TGC       378
78   Glu Lys Phe Val Lys Thr Val Glu Asp Lys Tyr Lys Cys Glu Lys Cys
79                   45                  50                  55
80
81   CAC CTG GTG CTG TGC AGC CCG AAG CAG ACC GAG TGT GGG CAC CGC TTC       426
82   His Leu Val Leu Cys Ser Pro Lys Gln Thr Glu Cys Gly His Arg Phe
83               60                  65                  70
84
85   TGC GAG AGC TGC ATG GCG GCC CTG CTG AGC TCT TCA AGT CCA AAA TGT       474
86   Cys Glu Ser Cys Met Ala Ala Leu Leu Ser Ser Ser Ser Pro Lys Cys
87           75                  80                  85
88
89   ACA GCG TGT CAA GAG AGC ATC GTT AAA GAT AAG GTG TTT AAG GAT AAT       522
90   Thr Ala Cys Gln Glu Ser Ile Val Lys Asp Lys Val Phe Lys Asp Asn
91       90                  95                  100
92
93   TGC TGC AAG AGA GAA ATT CTG GCT CTT CAG ATC TAT TGT CGG AAT GAA       570
94   Cys Cys Lys Arg Glu Ile Leu Ala Leu Gln Ile Tyr Cys Arg Asn Glu
95   105                 110                 115                 120
96
97   AGC AGA GGT TGT GCA GAG CAG TTA ATG CTG GGA CAT CTG GTG CAT TTA       618
98   Ser Arg Gly Cys Ala Glu Gln Leu Met Leu Gly His Leu Val His Leu
99                   125                 130                 135
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INPUT SET: S3120.raw

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100
101   AAA AAT GAT TGC CAT TTT GAA GAA CTT CCA TGT GTG CGT CCT GAC TGC        666
102   Lys Asn Asp Cys His Phe Glu Glu Leu Pro Cys Val Arg Pro Asp Cys
103           140                 145                 150
104
105   AAA GAA AAG GTC TTG AGG AAA GAC CTG CGA GAC CAC GTG GAG AAG GCG        714
106   Lys Glu Lys Val Leu Arg Lys Asp Leu Arg Asp His Val Glu Lys Ala
107           155                 160                 165
108
109   TGT AAA TAC CGG GAA GCC ACA TGC AGC CAC TGC AAG AGT CAG GTT CCG        762
110   Cys Lys Tyr Arg Glu Ala Thr Cys Ser His Cys Lys Ser Gln Val Pro
111           170                 175                 180
112
113   ATG ATC GCG CTG CAG AAA CAC GAA GAC ACC GAC TGT CCC TGC GTG GTG        810
114   Met Ile Ala Leu Gln Lys His Glu Asp Thr Asp Cys Pro Cys Val Val
115   185                 190                 195                 200
116
117   GTG TCC TGC CCT CAC AAG TGC AGC GTC CAG ACT CTC CTG AGG AGC GAG        858
118   Val Ser Cys Pro His Lys Cys Ser Val Gln Thr Leu Leu Arg Ser Glu
119               205                 210                 215
120
121   TTG AGT GCA CAC TTG TCA GAG TGT GTC AAT GCC CCC AGC ACC TGT AGT        906
122   Leu Ser Ala His Leu Ser Glu Cys Val Asn Ala Pro Ser Thr Cys Ser
123               220                 225                 230
124
125   TTT AAG CGC TAT GGC TGC GTT TTT CAG GGG ACA AAC CAG CAG ATC AAG        954
126   Phe Lys Arg Tyr Gly Cys Val Phe Gln Gly Thr Asn Gln Gln Ile Lys
127               235                 240                 245
128
129   GCC CAC GAG GCC AGC TCC GCC GTG CAG CAC GTC AAC CTG CTG AAG GAG       1002
130   Ala His Glu Ala Ser Ser Ala Val Gln His Val Asn Leu Leu Lys Glu
131           250                 255                 260
132
133   TGG AGC AAC TCG CTC GAA AAG AAG GTT TCC TTG TTG CAG AAT GAA AGT       1050
134   Trp Ser Asn Ser Leu Glu Lys Lys Val Ser Leu Leu Gln Asn Glu Ser
135   265                 270                 275                 280
136
137   GTA GAA AAA AAC AAG AGC ATA CAA AGT TTG CAC AAT CAG ATA TGT AGC       1098
138   Val Glu Lys Asn Lys Ser Ile Gln Ser Leu His Asn Gln Ile Cys Ser
139               285                 290                 295
140
141   TTT GAA ATT GAA ATT GAG AGA CAA AAG GAA ATG CTT CGA AAT AAT GAA       1146
142   Phe Glu Ile Glu Ile Glu Arg Gln Lys Glu Met Leu Arg Asn Asn Glu
143               300                 305                 310
144
145   TCC AAA ATC CTT CAT TTA CAG CGA GTG ATA GAC AGC CAA GCA GAG AAA       1194
146   Ser Lys Ile Leu His Leu Gln Arg Val Ile Asp Ser Gln Ala Glu Lys
147               315                 320                 325
148
149   CTG AAG GAG CTT GAC AAG GAG ATC CGG CCC TTC CGG CAG AAC TGG GAG       1242
150   Leu Lys Glu Leu Asp Lys Glu Ile Arg Pro Phe Arg Gln Asn Trp Glu
151           330                 335                 340
152
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RAW SEQUENCE LISTING
PATENT APPLICATION *US/08/404,832*

INPUT SET: S3120.raw

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153   GAA GCA GAC AGC ATG AAG AGC AGC GTG GAG TCC CTC CAG AAC CGC GTG        1290
154   Glu Ala Asp Ser Met Lys Ser Ser Val Glu Ser Leu Gln Asn Arg Val
155   345             350                 355                 360
156
157   ACC GAG CTG GAG AGC GTG GAC AAG AGC GCG GGG CAA GTG GCT CGG AAC        1338
158   Thr Glu Leu Glu Ser Val Asp Lys Ser Ala Gly Gln Val Ala Arg Asn
159           365                 370                 375
160
161   ACA GGC CTG CTG GAG TCC CAG CTG AGC CGG CAT GAC CAG ATG CTG AGT        1386
162   Thr Gly Leu Leu Glu Ser Gln Leu Ser Arg His Asp Gln Met Leu Ser
163           380                 385                 390
164
165   GTG CAC GAC ATC CGC CTA GCC GAC ATG GAC CTG GGC TTC CAG GTC CTG        1434
166   Val His Asp Ile Arg Leu Ala Asp Met Asp Leu Gly Phe Gln Val Leu
167           395                 400                 405
168
169   GAG ACC GCC AGC TAC AAT GGA GTG CTC ATC TGG AAG ATT CGC GAC TAC        1482
170   Glu Thr Ala Ser Tyr Asn Gly Val Leu Ile Trp Lys Ile Arg Asp Tyr
171       410                 415                 420
172
173   AAG CGG CGG AAG CAG GAG GCC GTC ATG GGG AAG ACC CTG TCC CTT TAC        1530
174   Lys Arg Arg Lys Gln Glu Ala Val Met Gly Lys Thr Leu Ser Leu Tyr
175   425                 430                 435                 440
176
177   AGC CAG CCT TTC TAC ACT GGT TAC TTT GGC TAT AAG ATG TGT GCC AGG        1578
178   Ser Gln Pro Phe Tyr Thr Gly Tyr Phe Gly Tyr Lys Met Cys Ala Arg
179               445                 450                 455
180
181   GTC TAC CTG AAC GGG GAC GGG ATG GGG AAG GGG ACG CAC TTG TCG CTG        1626
182   Val Tyr Leu Asn Gly Asp Gly Met Gly Lys Gly Thr His Leu Ser Leu
183               460                 465                 470
184
185   TTT TTT GTC ATC ATG CGT GGA GAA TAT GAT GCC CTG CTT CCT TGG CCG        1674
186   Phe Phe Val Ile Met Arg Gly Glu Tyr Asp Ala Leu Leu Pro Trp Pro
187           475                 480                 485
188
189   TTT AAG CAG AAA GTG ACA CTC ATG CTG ATG GAT CAG GGG TCC TCT CGA        1722
190   Phe Lys Gln Lys Val Thr Leu Met Leu Met Asp Gln Gly Ser Ser Arg
191       490                 495                 500
192
193   CGT CAT TTG GGA GAT GCA TTC AAG CCC GAC CCC AAC AGC AGC AGC TTC        1770
194   Arg His Leu Gly Asp Ala Phe Lys Pro Asp Pro Asn Ser Ser Ser Phe
195   505                 510                 515                 520
196
197   AAG AAG CCC ACT GGA GAG ATG AAT ATC GCC TCT GGC TGC CCA GTC TTT        1818
198   Lys Lys Pro Thr Gly Glu Met Asn Ile Ala Ser Gly Cys Pro Val Phe
199               525                 530                 535
200
201   GTG GCC CAA ACT GTT CTA GAA AAT GGG ACA TAT ATT AAA GAT GAT ACA        1866
202   Val Ala Gln Thr Val Leu Glu Asn Gly Thr Tyr Ile Lys Asp Asp Thr
203               540                 545                 550
204
205   ATT TTT ATT AAA GTC ATA GTG GAT ACT TCG GAT CTG CCC GAT CCC          1911
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INPUT SET: S3120.raw

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206   Ile Phe Ile Lys Val Ile Val Asp Thr Ser Asp Leu Pro Asp Pro
207           555               560.              565
208
209   TGATAAGTAG CTGGGGAGGT GGATTTAGCA GAAGGCAACT CCTCTGGGGG ATTTGAACCG   1971
210
211   GTCTGTCTTC ACTGAGGTCC TCGCGCTCAG AAAAGGACCT TGTGAGACGG AGGAAGCGGC   2031
212
213   AGAAGGCGGA CGCGTGCCGG CGGGAGGAGC CACGCGAGAG CACACCTGAC ACGTTTTATA   2091
214
215   ATAGACTAGC CACACTTCAC TCTGAAGAAT TATTTATCCT TCAACAAGAT AAATATTGCT   2151
216
217   GTCAGAGAAG GTTTTCATTT TCATTTTTAA AGATCTAGTT AATTAAGGTG GAAAACATAT   2211
218
219   ATGCTAAACA AAAGAAACAT GATTTTTCTT CCTTAAACTT GAACACCAAA AAAACACACA   2271
220
221   CACACACACA CGTGGGGATA GCTGGACATG TCAGCATGTT AAGTAAAAGG AGAATTTATG   2331
222
223   ·AAATAGTA                                                         2339
224
225
226   (2) INFORMATION FOR SEQ ID NO:2:
227
228          (i) SEQUENCE CHARACTERISTICS:
229              (A) LENGTH: 567 amino acids
230              (B) TYPE: amino acid
231              (D) TOPOLOGY: linear
232
233          (ii) MOLECULE TYPE: protein
234
235          (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
236
237   Met Glu Ser Ser Lys Lys Met Asp Ser Pro Gly Ala Leu Gln Thr Asn
238    1               5                 10                  15
239
240   Pro Pro Leu Lys Leu His Thr Asp Arg Ser Ala Gly Thr Pro Val Phe
241           20                  25                  30
242
243   Val Pro Glu Gln Gly Gly Tyr Lys Glu Lys Phe Val Lys Thr Val Glu
244           35                  40                  45
245
246   Asp Lys Tyr Lys Cys Glu Lys Cys His Leu Val Leu Cys Ser Pro Lys
247           50                  55                  60
248
249   Gln Thr Glu Cys Gly His Arg Phe Cys Glu Ser Cys Met Ala Ala Leu
250    65                  70                  75                  80
251
252   Leu Ser Ser Ser Ser Pro Lys Cys Thr Ala Cys Gln Glu Ser Ile Val
253                   85                  90                  95
254
255   Lys Asp Lys Val Phe Lys Asp Asn Cys Cys Lys Arg Glu Ile Leu Ala
256                   100                 105                 110
257
258   Leu Gln Ile Tyr Cys Arg Asn Glu Ser Arg Gly Cys Ala Glu Gln Leu
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SEQUENCE VERIFICATION REPORT
PATENT APPLICATION   *US/08/404,832*

INPUT SET: S3120.raw

Line	Error	Original Text
27	Wrong application Serial Number	(A) APPLICATION NUMBER: US